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STIC Biotechnology Systems Branch

RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 101567,992
Source: TFW0
Date Processed by STIC: 10/23/06

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 4.4.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<http://www.uspto.gov/ebc/efs/downloads/documents.htm>), EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 01/14/05):
U.S. Patent and Trademark Office, Mail Stop Sequence, Customer Window, Randolph Building, 401 Dulany Street, Alexandria, VA 22314

Revised 01/10/06

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Raw Sequence Listing Error Summary

ERROR DETECTED

SUGGESTED CORRECTION

SERIAL NUMBER:

10/567,992

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 Wrapped Nucleic
Wrapped Aminos The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
- 2 Invalid Line Length The rules require that a line not exceed 72 characters in length. This includes white spaces.
- 3 Misaligned Amino
Numbering The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
- 4 Non-ASCII The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
- 5 Variable Length Sequence(s) _____ contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6 PatentIn 2.0
"bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 7 Skipped Sequences
(OLD RULES) Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
- 8 Skipped Sequences
(NEW RULES) Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence.
<210> sequence id number
<400> sequence id number
000
- 9 Use of n's or Xaa's
(NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 10 Invalid <213>
Response Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence
- 11 Use of <220>
→ Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses.
Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
- 12 PatentIn 2.0
"bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
- 13 Misuse of n/Xaa "n" can only represent a single nucleotide; "Xaa" can only represent a single amino acid

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IFWO

RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/567,992

DATE: 10/23/2006
TIME: 17:53:58

Input Set : A:\Sequence Listing in Computer Readable Form.txt
Output Set: N:\CRF4\10232006\J567992.raw

```

3 <110> APPLICANT: Stewart, Russell J
4      Kiser, Patrick F
5      Staynor, Richard S
7 <120> TITLE OF INVENTION: Crosslinking Within Coordination Complexes
9 <130> FILE REFERENCE: p01129-WO-00
C--> 11 <140> CURRENT APPLICATION NUMBER: US/10/567,992
C--> 11 <141> CURRENT FILING DATE: 2006-02-09
11 <150> PRIOR APPLICATION NUMBER: 60/494,349
12 <151> PRIOR FILING DATE: 2003-08-11
14 <160> NUMBER OF SEQ ID NOS: 9
16 <170> SOFTWARE: PatentIn version 3.2

```

ERRORED SEQUENCES

```

85 <210> SEQ ID NO: 5
86 <211> LENGTH: 10
87 <212> TYPE: PRT
88 <213> ORGANISM: Artificial
90 <220> FEATURE:
91 <223> OTHER INFORMATION: sequence for HIS-tag
93 <220> FEATURE:
94 <221> NAME/KEY: MISC_FEATURE
95 <222> LOCATION: (10)..(10)
96 <223> OTHER INFORMATION: linkage to a monomeric titin I28 Ig domain
98 <400> SEQUENCE: 5
100 Tyr Gly Tyr Gly His His His His His
B--> 101 1      10 5
154 <210> SEQ ID NO: 9
155 <211> LENGTH: 9
156 <212> TYPE: PRT
W--> 157 <212> TYPE: Artificial
S--> 157 <212> TYPE: Artificial
E--> 159 <220> FEATURE:
160 <223> OTHER INFORMATION: sequence for HIS-tag
162 <220> FEATURE:
163 <221> NAME/KEY: MISC_FEATURE
164 <222> LOCATION: (9)..(9)
166 <213> ORGANISM:
166 <400> SEQUENCE: 9
168 His His His Gly Tyr Gly His His His
169 1      5
B--> 170 ???

```

file:///C:/CRF4/Outhold/VsrJ567992.htm # 11 on error summary sheet.

10/23/2006

What is the source of genetic material? (pg. 1-2)
Corrected Blanks Needed

Invalid Response

10 identifier

See item 10

pls use numeric

for 213) See item 10 on error response # 11 on error summary sheet.

organism

sequence for HIS-tag

same error

The type of errors shown exist throughout the Sequence Listing. Please check subsequent sequences for similar errors.

Q delete

See item

11 on

error summary sheet.

RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/567,992

DATE: 10/23/2006
TIME: 17:53:59

Input Set : A:\Sequence Listing in Computer Readable Form.txt
Output Set: N:\CRF4\10232006\J567992.raw

E--> 172 77
E--> 174 ??
E--> 176 ??
E--> 178 P01129.WO.00.txt
E--> 180 Page 4

pls delete

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RAW SEQUENCE LISTING ERROR SUMMARY DATE: 10/23/2006
PATENT APPLICATION: US/10/567,992 TIME: 17:54:00

Input Set : A:\Sequence Listing in Computer Readable Form.txt
Output Set: N:\CRF4\10232006\J567992.raw

Invalid <213> Response:

Use of "Artificial" only as "<213> Organism" response is incomplete,
per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

Seq#:1,2,3,4,5,6,7,8

BEST AVAILABLE COPY**VERIFICATION SUMMARY**

PATENT APPLICATION: US/10/567,992

DATE: 10/23/2006

TIME: 17:54:00

Input Set : A:\Sequence Listing in Computer Readable Form.txt
Output Set: N:\CRF4\10232006\J567992.raw

L:11 M:270 C: Current Application Number differs, Replaced Current Application No
L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:101 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:5 ✓
L:112 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:6
L:157 M:280 W: Numeric Identifier already exists, Type not replaced.
L:157 M:310 E: (3) Wrong or Missing Sequence Type, numeric identifier <212>, for SEQ ID#:9
L:166 M:282 E: Numeric Field Identifier Missing, <213> is required. ← →
L:170 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:170 M:330 E: (2) Invalid Amino Acid Designator, NUMBER OF INVALID KEYS:1
L:172 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:9
L:172 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:172 M:330 E: (2) Invalid Amino Acid Designator, NUMBER OF INVALID KEYS:1
M:332 Repeated in SeqNo=9
L:174 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:174 M:330 E: (2) Invalid Amino Acid Designator, NUMBER OF INVALID KEYS:1
L:176 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:176 M:330 E: (2) Invalid Amino Acid Designator, NUMBER OF INVALID KEYS:1
L:178 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:178 M:330 E: (2) Invalid Amino Acid Designator, NUMBER OF INVALID KEYS:1
L:180 M:252 E: No. of Seq. differs, <211> LENGTH:Input:9 Found:10 SEQ:9 //